

ATTORNEY DOCKET NO. 14028.0295P1

SEQUENCE LISTING

<110> The Government of the United States of America, as represented by t  
Secretary, Department of Health and Human Services

NEVILLE, David  
WOO, Jung-Hee  
LIU, Yuan-Yi

<120> METHODS FOR EXPRESSION AND PURIFICATION  
OF IMMUNOTOXINS

<130> 14028.0295P1

<140> Unassigned  
<141> 2004-08-02

<150> 60/491,923  
<151> 2003-08-01

<160> 35

<170> FastSEQ for Windows Version 4.0

<210> 1  
<211> 22  
<212> PRT  
<213> H. sapiens

<400> 1  
Asp Val Thr Leu His Ala Asp Ala Ile His Arg Gly Gly Gly Gln Ile  
1 5 10 15  
Ile Pro Thr Ala Arg Arg  
20

<210> 2  
<211> 22  
<212> PRT  
<213> M. musculus

<400> 2  
Asp Val Thr Leu His Ala Asp Ala Ile His Arg Gly Gly Gly Gln Ile  
1 5 10 15  
Ile Pro Thr Ala Arg Arg  
20

<210> 3  
<211> 22  
<212> PRT  
<213> R. norvegicus

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<400> 3

Asp Val Thr Leu His Ala Asp Ala Ile His Arg Gly Gly Gly Gln Ile  
1 5 10 15  
Ile Pro Thr Ala Arg Arg  
20

<210> 4

<211> 22  
<212> PRT

<213> C. griseus

<400> 4

Asp Val Thr Leu His Ala Asp Ala Ile His Arg Gly Gly Gly Gln Ile  
1 5 10 15  
Ile Pro Thr Ala Arg Arg  
20

<210> 5

<211> 22  
<212> PRT  
<213> D. melanogaster

<400> 5

Asp Val Thr Leu His Ala Asp Ala Ile His Arg Gly Gly Gly Gln Ile  
1 5 10 15  
Ile Pro Thr Thr Arg Arg  
20

<210> 6

<211> 22  
<212> PRT  
<213> C. elegans

<400> 6

Asp Val Thr Leu His Ala Asp Ala Ile His Arg Gly Gly Gly Gln Ile  
1 5 10 15  
Ile Pro Thr Ala Arg Arg  
20

<210> 7

<211> 22  
<212> PRT  
<213> S. pombe

<400> 7

Asp Val Val Leu His Ala Asp Ala Ile His Arg Gly Gly Gly Gln Ile  
1 5 10 15  
Ile Pro Thr Ala Arg Arg  
20

<210> 8

<211> 22

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<212> PRT  
<213> *P. pastoris*

<400> 8  
Asp Val Thr Leu His Ala Asp Ala Ile His Arg Gly Gly Gly Gln Val  
1 5 10 15  
Ile Pro Thr Met Lys Arg  
20

<210> 9  
<211> 22  
<212> PRT  
<213> *S. cerevisiae*

<400> 9  
Asp Val Thr Leu His Ala Asp Ala Ile His Arg Gly Gly Gly Gln Ile  
1 5 10 15  
Ile Pro Thr Met Arg Arg  
20

<210> 10  
<211> 66  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 10  
gatgttaccc tgcacgcccga tgctatccac cgccgcggag gacaagtcat tccaaaccatg 60  
aagaga 66

<210> 11  
<211> 223  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 11  
actttaagt tcttaatttt gttcctcgta gaaaagaacgc atagataatt caaaatggca 60  
aaatgggtat gtgtttttt atagttcatg tgccgaacaa ctaccgtttt aacttcactg 120  
tcgatcagat gcgatccctt atggacaagg tgtccaaacgt ccgtaacatg tcggttattg 180  
cccacgttga tcacggtaag tccactttaa ctgactccct ggt 223

<210> 12  
<211> 250  
<212> DNA  
<213> Artificial Sequence

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&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 12

actttgaagt	tcttaatttt	gttcctcgta	gaaagaacgc	atagataatt	caaaatgggt	60
atgttttt	ttatagtta	tgtgccgaac	aactaccgtt	tcaagatggg	agccagccac	120
taacatctcc	tctagttaac	ttcactgtcg	atcagatgcg	atccctttag	gacaagggtga	180
ccaacgtccg	taacatgtcg	gttattgccc	acgttgcata	cggttaagtcc	actttaactg	240
actccctgg						250

&lt;210&gt; 13

&lt;211&gt; 2601

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 13

atggtaact	tcactgtcg	tcagatgcga	tcccttatgg	acaagggtgac	caacgtccgt	60
aacatgtcgg	ttattgccc	cgttgatcac	ggtaagtcca	ctttaactga	ctccctgg	120
caacgtccg	gtattatttc	tgctgccaag	gctggtgagg	cccgtttcac	tgatactaga	180
aaggacgagc	aagagagagg	tatcaccato	aagtctaccg	ccatttctt	gtactctgag	240
atgggtgacg	acgatgtcaa	ggagatcaag	cagaagactg	aaggtaacag	tttccttac	300
aacttaattg	actccccagg	tcacggttgc	ttctcttctg	aggtcaactgc	tgctctgcgt	360
gttactgacg	gtgttttgtt	cgtcggttgc	tgtgttgaag	gtgtctgtgt	tcaaactgag	420
accgtttgc	gtcaagctt	gggtgaaaaga	atcaagccag	ttgttgtcat	taacaagg	480
gaccgtgctc	ttttggagtt	gcaagttacc	aaggaggacc	tgtaccagtc	tttcgctaga	540
accgtcgagt	ccgtaaacgt	cgttatcgct	acttacactg	acaagaccat	tggtgacaac	600
caagtctacc	cagaacaggg	taccgtcgct	ttcggttca	gtctgcacgg	atggctt	660
accgttagac	agttcgccac	tagatactcc	aagaagttcg	gtgttgcacag	aatcaagatg	720
atggagcg	tgtggggaga	ctcttacttc	aacccaaaga	ccaagaaatg	gaccaacaag	780
gacaaggacg	ccgctggaaa	gcctttggag	cgtgccttca	acatgttctg	tttgaccc	840
atctccgtc	tgtttgtgc	catcatgaac	ttcaagaagg	atgaaattcc	agttctgttg	900
gagaaattgg	agatcaac	gaagcgttag	gagaaggagt	ttggagggtaa	ggctt	960
aaggttgtca	tgagaaagtt	cttgccagct	gccgacgctt	tgttgagat	gattttctt	1020
cacccat	ctccagtcac	cgctcaagct	tacagagccg	agactttgt	cgaagg	1080
tctgtatgacc	aattctgcat	tggtatcaga	gagtgtgacc	ctaaggctga	gctgatgg	1140
tacatttcca	agatgg	aacctccgac	aaaggtagat	tctacgcctt	cggtcg	1200
ttctccgt	ctgttaagtc	cggtcaaaag	gtcagaatcc	aaaggctctaa	ctac	1260
ggtaagaagg	aggacttgtt	catcaaggct	gttcaaagaa	ctgttttgc	atggaaaga	1320
accgtcgagc	ctattgacga	tgtcccagct	ggtaacattc	ttggtattgt	gggtatcgac	1380
cagttctgc	tgaagtctgg	tactcttact	accaacgaag	ccgctcacaa	catgaagg	1440
atgaaattct	ctgtctctcc	agttgtgca	gttgcgtt	aggtcaagaa	cgctaatgt	1500
ctgccc	tggttgaggg	tctgaagcgt	ttgtcca	ctgacccatg	tg	1560
tacatctccg	agtctgg	gcacattgtt	gctggactg	gtgagctgca	ttgaaatc	1620
tgtttgc	atctgcaaga	cgaccacgct	ggtgtccctc	tgaagattc	tcctcc	1680
gttacctacc	gtgagactgt	cactaacgaa	tcttccatga	ctgccc	caagtctc	1740
aacaagcata	acagaattt	cctgaaggct	caaccaattg	acgaggaatt	gtcttgg	1800
atcgaagaag	gtaagg	cccaagagac	gactttaaag	ccagagccag	aatcatgg	1860
gatgaatacg	gttggacgt	cactgatg	cc	agaaagatct	gg	1920

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actggtgcca	acttagttgt	tgaccagtct	aaggctgtcc	aataacttgca	cgagatcaag	1980
gactctgttg	ttgccggttt	ccaattggct	accaaggaag	gtccaaatttt	gggagaaaaac	2040
atgagatccg	tcagagtcaa	catcttggat	gttaccctgc	acgcccgtgc	tatccacaga	2100
ggtggaggac	aagtcatcattcc	aaccatgaag	agagttacct	acgcccgcctt	cctgttggct	2160
gagccagcta	tccaggagcc	tatcttcttg	gtggagatcc	aatgtccaga	aatgtccatt	2220
ggtggtatct	actctgtttt	gaacaagaag	agaggtcaag	ttatctctga	ggaacaaaga	2280
ccaggtaccc	cattgttcac	tgtcaaagct	tacttgcag	ttaacgagtc	attcggtttc	2340
accggtaac	tgagacaaggc	taccgctggt	caagcttcc	cacagatggt	gttcgaccac	2400
tggccaaca	tgaatggtaa	cccattggac	ccagcctcca	aggtcggtga	gattgttctt	2460
gctgccagaa	agagacaggg	tatgaaggag	aacgtccctg	gttatgaaga	gtactacgac	2520
aagttgtaaag	cttaatgttt	cattaactta	tttgtgtcgt	tcgtatgtct	atttacgtac	2580
ttaattcagt	gtattgtgt	t				2601

&lt;210&gt; 14

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 14

Ala His Val Asp His Gly Lys Ser Thr  
1 5

&lt;210&gt; 15

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 15

Asp Glu Gln Glu Arg Gly Ile Thr Ile Lys Ser Thr Ala  
1 5 10

&lt;210&gt; 16

&lt;211&gt; 896

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 16

Ala Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met Glu  
1 5 10 15  
Asn Phe Ala Ser Tyr His Gly Thr Lys Pro Gly Tyr Val Asp Ser Ile  
20 25 30

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Gln Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly Asn Tyr Asp  
     35                   40                   45  
 Asp Asp Trp Lys Gly Phe Tyr Ser Thr Asp Asn Lys Tyr Asp Ala Ala  
     50                   55                   60  
 Gly Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala Gly Gly  
     65                   70                   75                   80  
 Val Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys  
     85                   90                   95  
 Val Asp Asn Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr  
     100                   105                   110  
 Glu Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg Phe  
     115                   120                   125  
 Gly Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly  
     130                   135                   140  
 Ser Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu Gln Ala Lys Ala Leu  
     145                   150                   155                   160  
 Ser Val Glu Leu Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg Gly Gln  
     165                   170                   175  
 Asp Ala Met Tyr Glu Tyr Met Ala Gln Ala Cys Ala Gly Asn Arg Val  
     180                   185                   190  
 Arg Arg Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp  
     195                   200                   205  
 Val Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His  
     210                   215                   220  
 Gly Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Ala Lys Thr Val Ser  
     225                   230                   235                   240  
 Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu  
     245                   250                   255  
 Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn Pro  
     260                   265                   270  
 Val Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln  
     275                   280                   285  
 Val Ile Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr Ala Ala  
     290                   295                   300  
 Leu Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly  
     305                   310                   315                   320  
 Ala Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu  
     325                   330                   335  
 Ser Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val  
     340                   345                   350  
 Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn Leu  
     355                   360                   365  
 Phe Gln Val Val His Asn Ser Tyr Asn Arg Pro Ala Tyr Ser Pro Gly  
     370                   375                   380  
 His Lys Thr Gln Pro Phe Leu Pro Trp Asp Ile Gln Met Thr Gln Thr  
     385                   390                   395                   400  
 Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys  
     405                   410                   415  
 Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln Gln Lys  
     420                   425                   430  
 Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His  
     435                   440                   445  
 Ser Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr  
     450                   455                   460

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Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe  
 465 470 475 480  
 Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Ala Gly Gly Thr Lys  
 485 490 495  
 Leu Glu Ile Lys Gly Gly Ser Gly Gly Gly Ser Gly Gly  
 500 505 510  
 Gly Gly Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys  
 515 520 525  
 Pro Gly Ala Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe  
 530 535 540  
 Thr Gly Tyr Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu  
 545 550 555 560  
 Glu Trp Met Gly Leu Ile Asn Pro Tyr Lys Gly Val Ser Thr Tyr Asn  
 565 570 575  
 Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser  
 580 585 590  
 Thr Ala Tyr Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val  
 595 600 605  
 Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe  
 610 615 620  
 Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Gly Gly  
 625 630 635 640  
 Gly Ser Gly Gly Ser Gly Gly Ser Asp Ile Gln Met  
 645 650 655  
 Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr  
 660 665 670  
 Ile Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr  
 675 680 685  
 Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser  
 690 695 700  
 Arg Leu His Ser Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly  
 705 710 715 720  
 Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala  
 725 730 735  
 Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Ala Gly  
 740 745 750  
 Gly Thr Lys Leu Glu Ile Lys Gly Gly Ser Gly Gly Gly Gly  
 755 760 765  
 Ser Gly Gly Gly Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu  
 770 775 780  
 Leu Val Lys Pro Gly Ala Ser Met Lys Ile Ser Cys Lys Ala Ser Gly  
 785 790 795 800  
 Tyr Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Lys Gln Ser His Gly  
 805 810 815  
 Lys Asn Leu Glu Trp Met Gly Leu Ile Asn Pro Tyr Lys Gly Val Ser  
 820 825 830  
 Thr Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Val Asp Lys  
 835 840 845  
 Ser Ser Ser Thr Ala Tyr Met Glu Leu Leu Ser Leu Thr Ser Glu Asp  
 850 855 860  
 Ser Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp  
 865 870 875 880  
 Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Leu Thr Val Phe Ser  
 885 890 895

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<210> 17  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<221> misc\_feature  
<222> 15  
<223> S = G or C

<400> 17  
ggggsggggs ggggs 15

<210> 18  
<211> 16  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<221> misc\_feature  
<222> 4,8,12,16  
<223> s = g or c

<400> 18  
gggsgggsggg gsggggs 16

<210> 19  
<211> 3  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<221> VARIANT  
<222> 2  
<223> Xaa= any amino acid

<221> VARIANT  
<222> 3  
<223> Xaa = s or t

<400> 19  
Asn Xaa Xaa  
1

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<210> 20  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 20  
ttggttattg accaaactaa ggctgtccaa 30

<210> 21  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 21  
acctctcttc ttgtttaaga cggagtagat 30

<210> 22  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 22  
cttgcttttg cggccgcctt tttttttttt tttttttttt 39

<210> 23  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 23  
gataagaatg cggccgcctt ttcttggctt ttgggttgaa g 41

<210> 24  
<211> 42  
<212> DNA  
<213> Artificial Sequence

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<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 24  
gataagaatg cggccgccaa cttagttgtt gaccagtcta ag 42

<210> 25  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 25  
atagcttagca ctttgaagtt cttaattttg ttcctc 36

<210> 26  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 26  
ataagaatgc ggccgcaagt taatgaaaca ttaagcttac aac 43

<210> 27  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 27  
gaatgacttg tcctccacc 19

<210> 28  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

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<400> 28  
gaatgacttg tcctccgcgg 20

<210> 29  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 29  
caactagcta gcgctcacaa catgaaggtc atgaaattc 39

<210> 30  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 30  
agaaccgtcg agcctattga cgat 24

<210> 31  
<211> 56  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 31  
ccctgcacgc cgatgctatc cacagaagag gaggacaagt cattccaacc atgaag 56

<210> 32  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 32  
gccgatgcta tccacagaag a 21

<210> 33  
<211> 21

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 33

gccgatgcta tccaccggccg c

21

<210> 34

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 34

tctcttcttg ttcaaaacag agtagatacc

30

<210> 35

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<221> misc\_feature

<222> 7,15

<223> n = g,a, c or t(u)

<400> 35

gtatgtncac taacntag

18